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Comparative genomic analysis of mycobacteriophages Krili, Corazon, Kanye, Nitzel, and Smooch

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Mycobacteriophages (hereafter referred to as phages) are ubiquitous viruses that infect mycobacteria. They have potential uses in the field of biotechnology and medical science with applications ranging from disease diagnosis, through phage typing, phage vaccine and phage therapy. Meanwhile, only a meager number of phages have been identified and characterized out of the multitudes present in the biosphere. In addition, a far majority of the bacteriophage genes that are discovered have no known function. In this study, five novel phages namely, Krili, Corazon, Kanye, Nitzel, and Smooch were annotated per the most recent guidelines using both PECAAN and DNA Master. While Krili was isolated and characterized at Purdue University, the other four phages were adopted from other institutions (see PhagesDB.org) for annotation. Of the characterized phages, Nitzel, classified as a cluster F phage, has the smallest genome size of 54kbp, and GC content of 61.3%. Corazon, a cluster S phage with genome size 65kbp has a GC content of 63.4%; Krili and Smooch from cluster O, both have a genome size of 71kbp and a GC content of 65.4%; while Kanye, a cluster E phage has a genome size of 75kbp and GC content of 63.1%. All five phages have the Siphoviridae morphotype. Only Kanye has a temperate life cycle, while the other four have the lytic life cycle. The right arm of Nitzel is characterized by many small genes, most with an overlap of 4 bp. Kanye has two tRNAs, while Nitzel has only one tRNA. Corazon, Krili, and Smooch have no tRNA. The cluster O phages, Krili and Smooch have their genomes flanked by reverse genes on the 5’ and 3’ ends. Corazon has two holin genes with each located downstream of each lysin gene, while Krili, Nitzel, Kanye and Smooch have only one holin gene. Structural genes such as terminase, portal, capsid maturation protease, scaffolding, major capsid, head-to-tail adaptor, major tail, tail assembly chaperone, and tape measure proteins were located in the 5’ upstream region of the genomes of Nitzel and Kanye. However, for the genome of Corazon, Krili and Smooch, these structural proteins are located in the middle of the genome. Corazon also has an unusual gene organization with some of its minor tail proteins located in the far right arm of the genome. The genomes of Smooch, Krili, Nitzel, Corazon and Kanye have 88 (70%), 88 (68%), 55 (56%), 75 (67%) and 82 (58%) genes with no known function respectively. Nitzel and Kanye have more members in their phage clusters and a lower frequency of genes with unknown function. The clusters of Smooch, Krili and Corazon have fewer members which may explain the higher frequency of genes with no known function in comparison to Nitzel and Kanye.